

0590

10/8

#5



OIPE

RAW SEQUENCE LISTING

DATE: 10/21/2002

PATENT APPLICATION: US/10/054,678

TIME: 17:05:10

Input Set : A:\2825.2012-004 Sequence Listing.txt

Output Set: N:\CRF4\10212002\J054678.raw

ENTERED

4 <110> APPLICANT: Sklar, Pamela
5 Lander, Eric S.
6 McInnis, Melvin G.
7 DePaulo, Jr., J. Raymond
8 Willour, Virginia
9 Potash, James
11 <120> TITLE OF INVENTION: ASSOCIATION OF DOPAMINE BETA-HYDROXYLASE
12 POLYMORPHISMS WITH BIPOLAR DISORDER
15 <130> FILE REFERENCE: 2825.2012-004
17 <140> CURRENT APPLICATION NUMBER: US 10/054,678
18 <141> CURRENT FILING DATE: 2002-01-22
20 <150> PRIOR APPLICATION NUMBER: US 09/852,967
21 <151> PRIOR FILING DATE: 2001-05-10
23 <150> PRIOR APPLICATION NUMBER: US 60/202,910
24 <151> PRIOR FILING DATE: 2000-05-10
26 <160> NUMBER OF SEQ ID NOS: 2
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2725
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 1
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38 agagccccct cccctatcac atccccctgg acccgaggag gtccctggag ctctcatgga 180
39 atgtcagcta caccagagag gccatccatt tccagctcct ggtgcggagg ctcaaggctg 240
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44 gcaactgtcca cttgggtctac gggatccttg aggagccgtt ccggtcactg gaggccatca 540
45 acggctcggg cctgcagatg gggtgcaga gggtgcagct cctgaagccc aatatccccg 600
46 aaccggaggt gccctcagac gcgtgcacca tggaggtcca agctcccaat atccagatcc 660
47 ccagccagga gaccacgtac tgggtgtaca ttaaggagct tccaaagggc ttctctcggc 720
48 accacattat caagtacgag cccatcgtca ccaagggcaa tgaggccctt gtccaccaca 780
49 tgggaagtct ccagtgcgc cccgagatgg acagcgtccc ccacttcagc gggccctgcg 840
50 actccaagat gaaacccgac cgcctcaact actgcccga cgtgctggcc gcctgggccc 900
51 tgggtgccaa ggcatcttac taccagagg aagccggcct tgccttcggg ggtccagggt 960
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57 tgggtccggga cggccgggag tgggagatcg tgaaccagga caatcactac agccctcact 1320
58 tccaggagat ccgcatgttg aagaaggctg tgtcgggtcca tccgggagat gtgctcatca 1380
59 cctcctgcac gtacaacacg gaagaccggg agctggccac agtggggggc ttcgggatcc 1440
60 tggaggagat gtgtgtcaac tacgtgcact actaccccca gacgcagctg gagctctgca 1500
61 agacggctgt ggacgcccgc ttctgtcaga agtacttcca cctcatcaac aggttcaaca 1560
62 acgaggatgt ctgcacctgc cctcaggcgt ccgtgtctca gcagttcacc tctgttccct 1620
63 ggaactcctt caaccgcgac gtactgaagg ccctgtacag cttcgcgccc atctccatgc 1680
64 actgcaacaa gtcctcagcc gtccgcttcc aggttgaatg gaacctgcag cccctgccc 1740
65 aggtcatctc cacactggaa gagccacccc cacagtgcac caccagccag ggccgaagcc 1800
66 ctgctggccc caccgttgtc agcattgggtg ggggcaaagg ctgagggggg acctactcct 1860
67 cccctcctc catgctgtcc ctgtgggctc acaccggcac tgtgcactct actctgcgac 1920
68 gatccccatg gaacagccct gcacgcccag gatgaagggg ccagaccacg cccctgcctg 1980
69 agaccacggt ccaatccagc cttcttcccc cagggtcccc tgcattggctg agagggtgtg 2040
70 ggtgccctgt tgacctaccc tggaccgagt ggaccacgac ctctgccatt taaaccggc 2100
71 tgactcagtg cagggacagc ccgcacagtg gtccagggtc cagccctccg ccagccctgt 2160
72 tccgcctcac tgggtgtggc ctggcttctg ggacaggcac catgctgggc cggggtgtgg 2220
73 aatcaccggg aacgcccccg ccccgcccc gctgctcccg gtgtgcagcg ggtgcgggtg 2280
74 ccgcttaaac atttccctgc tgagtggctc gtgtttcaca gtgggcggtc tccctgcgac 2340
75 ggaggcagga ccaggcattt agctagttag agactgcctt gggaaattgc tccattcctg 2400
76 agtaaacaga tattttogcc cacctaaagg gaagccctga caacaactat caccaaaaga 2460
77 cgaggcggca aagatccagc ggggcttctg ggcgcgggtt ccacgtgggg tgggaattatt 2520
78 agcaccagct tgcttctctg ccggtggggc cagcgctgaa cagaccgggg tggagtcagg 2580
79 gctgtgcttt ccgctgtggt ctgccactta gggagtgtgc cttgggcggg ccatttcaca 2640
80 ttcttgacct tcaattttct catctgtaaa accaggctga tgccgtgcgg gctaattgac 2700
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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 603

85 <212> TYPE: PRT

86 <213> ORGANISM: Homo sapiens

88 <400> SEQUENCE: 2

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89 Met Arg Glu Ala Ala Phe Met Tyr Ser Thr Ala Val Ala Ile Phe Leu
90 1 5 10 15
91 Val Ile Leu Val Ala Ala Leu Gln Gly Ser Ala Pro Arg Glu Ser Pro
92 20 25 30
93 Leu Pro Tyr His Ile Pro Leu Asp Pro Glu Gly Ser Leu Glu Leu Ser
94 35 40 45
95 Trp Asn Val Ser Tyr Thr Gln Glu Ala Ile His Phe Gln Leu Leu Val
96 50 55 60
97 Arg Arg Leu Lys Ala Gly Val Leu Phe Gly Met Ser Asp Arg Gly Glu
98 65 70 75 80
99 Leu Glu Asn Ala Asp Leu Val Val Leu Trp Thr Asp Gly Asp Thr Ala
100 85 90 95
101 Tyr Phe Ala Asp Ala Trp Ser Asp Gln Lys Gly Gln Ile His Leu Asp
102 100 105 110
103 Pro Gln Gln Asp Tyr Gln Leu Leu Gln Val Gln Arg Thr Pro Glu Gly
104 115 120 125
105 Leu Thr Leu Leu Phe Lys Arg Pro Phe Gly Thr Cys Asp Pro Lys Asp
106 130 135 140
107 Tyr Leu Ile Glu Asp Gly Thr Val His Leu Val Tyr Gly Ile Leu Glu

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108 145          150          155          160
109 Glu Pro Phe Arg Ser Leu Glu Ala Ile Asn Gly Ser Gly Leu Gln Met
110          165          170          175
111 Gly Leu Gln Arg Val Gln Leu Leu Lys Pro Asn Ile Pro Glu Pro Glu
112          180          185          190
113 Leu Pro Ser Asp Ala Cys Thr Met Glu Val Gln Ala Pro Asn Ile Gln
114          195          200          205
115 Ile Pro Ser Gln Glu Thr Thr Tyr Trp Cys Tyr Ile Lys Glu Leu Pro
116          210          215          220
117 Lys Gly Phe Ser Arg His His Ile Ile Lys Tyr Glu Pro Ile Val Thr
118 225          230          235          240
119 Lys Gly Asn Glu Ala Leu Val His His Met Glu Val Phe Gln Cys Ala
120          245          250          255
121 Pro Glu Met Asp Ser Val Pro His Phe Ser Gly Pro Cys Asp Ser Lys
122          260          265          270
123 Met Lys Pro Asp Arg Leu Asn Tyr Cys Arg His Val Leu Ala Ala Trp
124          275          280          285
125 Ala Leu Gly Ala Lys Ala Phe Tyr Tyr Pro Glu Glu Ala Gly Leu Ala
126          290          295          300
127 Phe Gly Gly Pro Gly Ser Ser Arg Tyr Leu Arg Leu Glu Val His Tyr
128 305          310          315          320
129 His Asn Pro Leu Val Ile Glu Gly Arg Asn Asp Ser Ser Gly Ile Arg
130          325          330          335
131 Leu Tyr Tyr Thr Ala Lys Leu Arg Arg Phe Asn Ala Gly Ile Met Glu
132          340          345          350
133 Leu Gly Leu Val Tyr Thr Pro Val Met Ala Ile Pro Pro Arg Glu Thr
134          355          360          365
135 Ala Phe Ile Leu Thr Gly Tyr Cys Thr Asp Lys Cys Thr Gln Leu Ala
136          370          375          380
137 Leu Pro Pro Ser Gly Ile His Ile Phe Ala Ser Gln Leu His Thr His
138 385          390          395          400
139 Leu Thr Gly Arg Lys Val Val Thr Val Leu Val Arg Asp Gly Arg Glu
140          405          410          415
141 Trp Glu Ile Val Asn Gln Asp Asn His Tyr Ser Pro His Phe Gln Glu
142          420          425          430
143 Ile Arg Met Leu Lys Lys Val Val Ser Val His Pro Gly Asp Val Leu
144          435          440          445
145 Ile Thr Ser Cys Thr Tyr Asn Thr Glu Asp Arg Glu Leu Ala Thr Val
146          450          455          460
147 Gly Gly Phe Gly Ile Leu Glu Glu Met Cys Val Asn Tyr Val His Tyr
148 465          470          475          480
149 Tyr Pro Gln Thr Gln Leu Glu Leu Cys Lys Thr Ala Val Asp Ala Gly
150          485          490          495
151 Phe Leu Gln Lys Tyr Phe His Leu Ile Asn Arg Phe Asn Asn Glu Asp
152          500          505          510
153 Val Cys Thr Cys Pro Gln Ala Ser Val Ser Gln Gln Phe Thr Ser Val
154          515          520          525
155 Pro Trp Asn Ser Phe Asn Arg Asp Val Leu Lys Ala Leu Tyr Ser Phe
156          530          535          540

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157	Ala	Pro	Ile	Ser	Met	His	Cys	Asn	Lys	Ser	Ser	Ala	Val	Arg	Phe	Gln
158	545					550					555					560
159	Gly	Glu	Trp	Asn	Leu	Gln	Pro	Leu	Pro	Lys	Val	Ile	Ser	Thr	Leu	Glu
160					565					570						575
161	Glu	Pro	Thr	Pro	Gln	Cys	Pro	Thr	Ser	Gln	Gly	Arg	Ser	Pro	Ala	Gly
162					580					585					590	
163	Pro	Thr	Val	Val	Ser	Ile	Gly	Gly	Gly	Lys	Gly					
164			595													600

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/054,678

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TIME: 17:05:11

Input Set : A:\2825.2012-004 Sequence Listing.txt

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